LISTING OF THE CLAIMS

1. (Previously presented) A method of identifying a compound that binds to a coactivator binding site of a nuclear receptor, said method comprising:

modeling a test compound that fits spatially into the nuclear receptor coactivator binding site using an atomic structural model of the nuclear receptor coactivator binding site or portion thereof; and

screening said test compound in an assay that measures binding of the test compound to the nuclear receptor coactivator binding site, thereby identifying a test compound that binds to the coactivator binding site of said nuclear receptor.

2. (Previously presented) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with residues selected from the group consisting of Val284, Phe293, Ile302, Leu305, and Leu454 found in a portion of human thyroid beta receptor, the portion represented by SEQ ID NO: 52 or SEQ ID NO: 53.

3. (Previously presented) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with residues selected from the group consisting of Val284, Lys288, Ile302, Lys306, Leu454 and Glu457 found in a portion of human thyroid beta receptor, the portion represented by SEQ ID NO: 52 or SEQ ID NO: 53.

4. (Previously presented) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Ile280, Thr281, Val283, Val284, Ala287, Lys288, helix 4 residue Phe293, helix 5 residues Gln301, Ile302, Leu305, Lys306, helix 6 residue Cys309, helix 12 residues Pro453, Leu454, Glu457, Val458, and Phe459 found in a portion of human thyroid beta receptor, the portion represented by SEQ ID NO: 52 or SEQ ID NO: 53.

5. (Previously presented) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Ile280, Thr281, Val283, Val284, Ala287, and Lys288, helix 4 residue Phe293, helix 5 residues Gln301, Ile302, Leu305, Lys306, helix 6 residue Cys309, and helix 12 residues Pro453, Leu454, Glu457,

Val458 and Phe459 found in a portion of human thyroid beta receptor, the portion represented by SEQ ID NO: 52 or SEQ ID NO: 53.

6. (Previously presented) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of Val284, Phe293, Ile302, Leu305, and Leu454 found in a portion of human thyroid beta receptor, the portion represented by SEQ ID NO: 52 or SEQ ID NO: 53.

7. (Previously presented) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of Val284, Lys288, Ile302, Lys306, Leu454 and Glu457 found in a portion of human thyroid beta receptor, the portion represented by SEQ ID NO: 52 or SEQ ID NO: 53.

8. (Previously presented) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with helix 3 residues selected from the group consisting of Ile280, Val283, Val284, Ala287, helix 4 residue Phe293, helix 5 residues, Ile302, Leu305, helix 6 residue Cys309, and helix 12 residues Leu454, Val458 and Phe459 found in a portion of human thyroid beta receptor, the portion represented by SEQ ID NO: 52 or SEQ ID NO: 53.

9. (Previously presented) The method of any one of claims 5 through 8, wherein said nuclear receptor is selected from the group consisting of receptors for thyroid hormones, retinoids, peroxisomes, vitamin D, estrogens, glucocorticoids, progestins, mineralocorticoids and androgens.

10. (Original) The method of claim 1, wherein said screening is in vitro.

11. (Original) The method of claim 10, wherein said screening is high throughput screening.

12. (Previously presented) The method of claim 1, wherein said assay is an *in vivo* assay.

13. (Original) The method of claim 1, wherein said test compound is from a library of compounds.

14. (Original) The method of claim 1, wherein said test compound is an agonist or antagonist of coactivator binding.

15. (Previously presented) The method of claim 14, wherein said test compound is a small organic molecule, a peptide, or a peptidomimetic.

16. (Previously presented) The method of Claim 15, wherein the test compound is a peptide comprising a nuclear receptor box amino acid sequence or derivative thereof.

17 – 29. (Cancelled)

30. (Previously presented) A compound identified according to the method of claim 1.

31. (Previously presented) The method of Claim 1 wherein the atomic coordinates of the nuclear receptor coactivator binding site are provided to a computerized modeling system.

32. (Previously presented) The method of claim 14 wherein the agonist promotes hormone-dependent coactivator binding to the receptor.

33. (Previously presented) The method of claim 14 wherein the antagonist blocks hormone-dependent coactivator binding to the receptor.

34. (Withdrawn) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with helix 3 residues Leu354, Val355, Met357, Ile358, Ala361, and Lys362, helix 4 residue Phe367, helix 5 residues Gln375, Val376, Leu379, Glu380, helix 6 residue Trp383, and helix 12 residues Asp538, Leu539, Glu542, Met543 and Leu544 found in a portion of human estrogen alpha receptor (SEQ ID NO: 56, SEQ ID NO: 57 or SEQ ID NO: 60).

35. (Withdrawn) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Leu354, Val355, Met357, Ile358, Ala361, and Lys362, helix 4 residue Phe367, helix 5 residues Gln375, Val376, Leu379, Glu380, helix 6 residue Trp383, and helix 12 residues Asp538, Leu539, Glu542, Met543 and Leu544 found in a portion of human estrogen alpha receptor (SEQ ID NO: 56, SEQ ID NO: 57 or SEQ ID NO: 60).

36. (Withdrawn) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Ile238, Ile239, Ile241, Val242, Ala245, and Lys246, helix 4 residue Phe251, helix 5 residues Gln259, Ile260, Leu263, Lys264, helix 6 residue Cys267, and helix 12 residues Pro410, Leu411, Glu414, Met415 and Leu416 found in a portion of human retinoid receptor hRARγ (SEQ ID NO: 34 and SEQ ID NO: 35).

37. (Withdrawn) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Leu276, Phe277, Leu279, Val280, Ala283, and Lys284, helix 4 residue Phe289, helix 5 residues Gln297, Val298, Leu301, Arg302, helix 6 residue Trp305, and helix 12 residues Thr449, Phe450, Glu453, Met454 and Leu455 found in a portion of human retinoid receptor hRXRα (SEQ ID NO: 36 and SEQ ID NO: 37).

38. (Withdrawn) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Val291, Glu292, Ile294, Thr295, Ala298, and Lys299, helix 4 residue Phe304, helix 5 residues Gln312, Val313, Leu316, Lys317, helix 6 residue Val320, and helix 12 residues Pro465, Leu466, Glu469, Ile470 and Tyr471 found in a portion of human peroxisome receptor hPPARγ (SEQ ID NO: 36 and SEQ ID NO: 37).

39. (Withdrawn) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Ile238, Glu239, Val241, Ile242, Ala245, and Lys246, helix 4 residue Phe251, helix 5 residues Gln259, Val260, Leu263, Lys264, helix 6 residue Ala267, and helix 12 residues Pro416, Leu417, Glu420, Val421 and Phe422 found in a portion of human vitamin D receptor hVDR (SEQ ID NO: 40 and SEQ ID NO: 41).

40. (Withdrawn) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Val571, Ile572, Ala574, Val575, Ala578, and Lys579, helix 4 residue Phe584, helix 5 residues Gln592, Met593,

Leu596, Gln597, helix 6 residue Trp600, and helix 12 residues Glu751, Met752, Glu755, Ile756 and Ile757 found in a portion of human glucocorticoid receptor hGR (SEQ ID NO: 44 and SEQ ID NO: 45).

41. (Withdrawn) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Val726, Ile727, Ala729, Val730, Ala733, and Lys734, helix 4 residue Phe739, helix 5 residues Gln747, Met748, Leu751, Gln752, helix 6 residue Trp755, and helix 12 residues Glu907, Met908, Glu911, Ile912 and Ile913 found in a portion of human progestin receptor hPR (SEQ ID NO: 46 and SEQ ID NO: 47).

42. (Withdrawn) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Met777, Ile778, Val780, Val781, Ala784, and Lys785, helix 4 residue Phe790, helix 5 residues Gln798, Ile799, Ile802, Gln803, helix 6 residue Trp806, and helix 12 residues Ala958, Met959, Glu962, Ile963 and Ile964 found in a portion of human mineralocorticoid receptor hMR (SEQ ID NO: 48 and SEQ ID NO: 49).

43. (Withdrawn) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues selected from the group consisting of helix 3 residues Leu245, Val246, Val248, Val249, Ala252, and Lys253, helix 4 residue Phe258, helix 5 residues Gln266, Met267, Ile270, Gln271, helix 6 residue Trp274, and helix 12 residues Glu426, Met427, Glu430, Ile431 and Ile432 found in a portion of human androgen receptor hAR (SEQ ID NO: 50 and SEQ ID NO: 51).

Claims 44 – 50. (Cancelled).

51. (Previously presented) The method of claim 1, wherein the atomic structural model comprises the set of structure coordinates depicted in Appendix 1, or a homologue thereof, the homologue having a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

52. (Previously presented) The method of claim 1 wherein the atomic structural model is experimentally derived.

53. (Previously presented) The method of claim 1, wherein said atomic structural model additionally comprises atomic coordinates of a molecule bound to the coactivator binding site.

54. (Previously presented) The method of claim 53 wherein the molecule is a peptide.

55. (Previously presented) The method of claim 54 wherein the peptide comprises a nuclear receptor box sequence.

56. (Previously presented) The method of claim 54 wherein the peptide consists of a portion of GRIP1 comprising a nuclear receptor box 2 sequence.

57. (Previously presented) The method of claim 54 wherein the peptide consists of a portion of GRIP1 comprising a nuclear receptor box 3 sequence.

58. (Previously presented) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues that form a hydrophobic cleft of the coactivator binding site.

59. (Previously presented) The method of claim 58 wherein the test compound interacts with the amino acid residues.

60. (Previously presented) The method of claim 58 wherein the test compound interacts with at least one of the amino acid residues.

61. (Previously presented) The method of any one of claims 2 – 8 wherein the test compound interacts with amino acid residues that form a hydrophobic cleft in the coactivator binding site.

62. (Previously presented) The method of any one of claims 2 – 8 wherein the test compound interacts with the amino acid residues.